S/N 09/804866

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (currently amended) A method of analyzing argentinated peptides or argentinated proteins using mass spectrometry comprising: (a) combining an oligopeptide with silver to provide a sample comprising argentinated ~~argentiated~~ oligopeptide; (b) submitting the sample to a mass spectrometer; (c) performing scans of silver containing peaks in optimum collision energies to maximize doublet or triplet peak patterns, wherein the scans are performed: (i) under increasing collision energies, identifying doublet and triplet peak patterns and determining the collision energies that maximize the doublet and/or triplet peak patterns, summing the spectra information from said optimum collision energies to produce a composite spectra that maximizes the doublet and/or triplet peak patterns; or (ii) over a range of collision energies to maximize the doublet and/or triplet peak patterns; (d) identifying any doublet or triplet peak pattern; (e) confirming with Y ions; and (f) determining partial sequence by the mass separation between two successive doublet or triplet patterns.

2. (currently amended) A method according to claim 1 wherein the performing scans comprises collecting product ion spectra of the $[M+Ag]^+$ ion, where M=oligopeptide. [[;]]

3. (currently amended) A method according to claim 1 wherein the oligopeptide consists of ~~comprises~~ from about 3 to about 10 amino acids.

4. (previously presented) A method according to claim 1 wherein the silver is silver nitrate.

4

S/N 09/804866

5. (currently amended) A method according to claim 1, wherein the ~~step of determining~~ ~~determination of~~ partial sequence by the mass separation between two successive doublet or triplet patterns further comprises searching for, and identifying cleaved amino acid residues based on differences in m/z values of neighboring triplets where the m/z value of the $[b_n - H + Ag]^+$ ion and the corresponding $[y_n + H + Ag]^+$ ion are related by the formula: $|y_n + H + Ag]^+ = [M + Ag]^+ + Ag^+ - [b_n - H + Ag]^+$.

6. (original) A method according to claim 5 wherein the searching and identifying is conducted by a custom search algorithm.

7. (currently amended) A method according to claim 6 wherein the algorithm is written in Visual Basic and identifies both ~~looks for~~ the triplet peak pattern of $(m/z)_1$, $(m/z)_2 = (m/z)_1 - 18.0$, and $(m/z)_3 = (m/z)_2 - 28.0$ as well as the doublet pattern of $(m/z)_2$ and $(m/z)_3$, all to within ± 0.5 m/z unit.

8. (currently amended) A method according to claim 2 ~~1~~ wherein product ion spectra of the $[M + Ag]^+$ ion are collected under E_{cm}s, of 1.5, 2.0, 2.5 and 3.0 eV.

9. (previously presented) A method according to claim 1 wherein the mass spectrometer is a triple quadrupole mass spectrometer, two triple quadrupole mass spectrometers, a quadrupole/time-of-flight mass spectrometer, an ion-trap mass spectrometer, or a time-of-flight mass spectrometer amenable to post-source decay or collision-induced dissociation.

10. (currently amended) A method of analyzing argentinated peptides or argentinated proteins using mass spectrometry comprising: (a) combining an oligopeptide with silver nitrate in solution; (b) submitting a sample of the solution to a mass spectrometer; (c) collecting product ion spectra of the $[M+Ag]^+$ ion, where M=oligopeptide; (d) identifying a triplet peak pattern; (e) identifying a doublet peak pattern; and (f) searching for, and identifying cleaved amino acid residues based on differences in m/z values of neighboring triplets where the m/z value of the

5

S/N 09/804866

$[b_n-H+Ag]^+$ ion and the corresponding $[y_n+H+Ag]^+$ ion are related by the formula:
$[y_n+H+Ag]^+=[M+Ag]^++Ag^+-[b_n-H+Ag]^+$.

11. (currently amended) A method according to claim 10 wherein the oligopeptide <u>consists of</u> ~~comprises~~ from about 3 to about 10 amino acids.

12. (previously presented) A method according to claim 10 wherein the searching and identifying is conducted by a custom search algorithm.

13. (original) A method according to claim 12 wherein the algorithm is written in Visual Basic and looks for the triplet peak pattern of $(m/z)_1$, $(m/z)_2=(m/z)_1-18.0$, and $(m/z)_3=(m/z)_2-28.0$ as well as the doublet pattern of $(m/z)_2$ and $(m/z)_3$, all to within +- 0.5 m/z unit.

14. (previously presented) A method according to claim 10 wherein product ion spectra of the $[M + Ag]^+$ ion are collected under E_{cm}s, of 1.5, 2.0, 2.5 and 3.0 eV.

15. (previously presented) A method according to claim 10 wherein the mass spectrometer is a triple quadrupole mass spectrometer, two triple quadrupole mass spectrometers, a quadrupole/ time-of-flight mass spectrometer, an ion-trap mass spectrometer, or a time-of-flight mass spectrometer amenable to post-source decay or collision-induced dissociation.

6